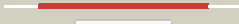



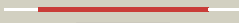

















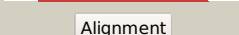





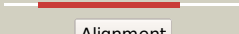












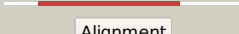
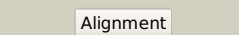
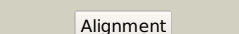



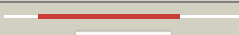


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1552_(frdA)_1757687_1759438
Date	Fri Aug 2 13:30:14 BST 2019
Unique Job ID	6fdcf78b440f2a02

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3vr8E_</a>	 Alignment		100.0	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> flavoprotein subunit of complex ii; <b>PDBTitle:</b> mitochondrial rho-ubiquinol-fumarate reductase from the parasitic nematode ascaris suum
2	<a href="#">c1yq4A_</a>	 Alignment		100.0	40	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> succinate dehydrogenase flavoprotein subunit; <b>PDBTitle:</b> avian respiratory complex ii with 3-nitropropionate and ubiquinone
3	<a href="#">c1kf6A_</a>	 Alignment		100.0	54	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate reductase flavoprotein; <b>PDBTitle:</b> e. coli quinol-fumarate reductase with bound inhibitor hqno
4	<a href="#">c3p4rM_</a>	 Alignment		100.0	54	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> fumarate reductase flavoprotein subunit; <b>PDBTitle:</b> crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
5	<a href="#">c5xmjE_</a>	 Alignment		100.0	39	<b>PDB header:</b> electron transport <b>Chain:</b> E: <b>PDB Molecule:</b> fumarate reductase flavoprotein subunit; <b>PDBTitle:</b> crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
6	<a href="#">c2bs3A_</a>	 Alignment		100.0	39	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> quinol-fumarate reductase flavoprotein subunit a; <b>PDBTitle:</b> glu c180 -> gln variant quinol:fumarate reductase from2 wolinella succinogenes
7	<a href="#">c2aczA_</a>	 Alignment		100.0	44	<b>PDB header:</b> oxidoreductase/electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> succinate dehydrogenase flavoprotein subunit; <b>PDBTitle:</b> complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site
8	<a href="#">c6n56A_</a>	 Alignment		100.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate reductase, flavo protein subunit; <b>PDBTitle:</b> crystal structure of fumarate reductase, flavo protein subunit, from2 helicobacter pylori g27
9	<a href="#">c3cirM_</a>	 Alignment		100.0	53	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> fumarate reductase flavoprotein subunit; <b>PDBTitle:</b> e. coli quinol fumarate reductase frda t234a mutation
10	<a href="#">c2fjaC_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> adenylylsulfate reductase, subunit a; <b>PDBTitle:</b> adenosine 5'-phosphosulfate reductase in complex with substrate
11	<a href="#">c3gyxA_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> adenylylsulfate reductase; <b>PDBTitle:</b> crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas

12	<a href="#">c1chuA</a>	 Alignment		100.0	35	<b>PDB header:</b> flavoenzyme <b>Chain:</b> A: <b>PDB Molecule:</b> protein (l-aspartate oxidase); <b>PDBTitle:</b> structure of l-aspartate oxidase: implications for the2 succinate dehydrogenase/ fumarate reductase family
13	<a href="#">c2e5vA</a>	 Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate oxidase; <b>PDBTitle:</b> crystal structure of l-aspartate oxidase from2 hyperthermophilic archaean sulfolobus tokodaii
14	<a href="#">c1qo8A</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c3 fumarate reductase; <b>PDBTitle:</b> the structure of the open conformation of a flavocytochrome c32 fumarate reductase
15	<a href="#">c1d4cB</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavocytochrome c fumarate reductase; <b>PDBTitle:</b> crystal structure of the uncomplexed form of the flavocytochrome c2 fumarate reductase of shewanella putrefaciens strain mr-1
16	<a href="#">c1jrxA</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavocytochrome c; <b>PDBTitle:</b> crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
17	<a href="#">c4c3yF</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> 3-ketosteroid dehydrogenase; <b>PDBTitle:</b> crystal structure of 3-ketosteroid delta1-dehydrogenase from2 rhodococcus erythropolis sq1 in complex with 1,4-androstadiene-3,17-3 dione
18	<a href="#">c4at2A</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-ketosteroid-delta4-5alpha-dehydrogenase; <b>PDBTitle:</b> the crystal structure of 3-ketosteroid-delta4-(5alpha)-2 dehydrogenase from rhodococcus jostii rha1 in complex3 with 4-androstene-3,17- dione
19	<a href="#">d1chua2</a>	 Alignment		100.0	37	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
20	<a href="#">c5glgA</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fumarate reductase 2; <b>PDBTitle:</b> the novel function of osm1 under anaerobic condition in the er was2 revealed by crystal structure of osm1, a soluble fumarate reductase3 in yeast
21	<a href="#">d1kf6a2</a>	 Alignment	not modelled	100.0	56	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
22	<a href="#">d1qo8a2</a>	 Alignment	not modelled	100.0	28	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
23	<a href="#">d1y0pa2</a>	 Alignment	not modelled	100.0	30	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
24	<a href="#">c3v76A</a>	 Alignment	not modelled	100.0	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> flavoprotein; <b>PDBTitle:</b> the crystal structure of a flavoprotein from sinorhizobium meliloti
25	<a href="#">c2gqfA</a>	 Alignment	not modelled	100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein hi0933; <b>PDBTitle:</b> crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
26	<a href="#">d1neka2</a>	 Alignment	not modelled	100.0	48	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
27	<a href="#">d2bs2a1</a>	 Alignment	not modelled	100.0	36	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
28	<a href="#">c2i0zA</a>	 Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad(fad)-utilizing dehydrogenases; <b>PDBTitle:</b> crystal structure of a fad binding protein from bacillus2

						cereus, a putative nad(fad)-utilizing dehydrogenases <b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
29	<a href="#">d1d4ca2</a>	Alignment	not modelled	100.0	30	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
30	<a href="#">d1neka1</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
31	<a href="#">d1kf6a1</a>	Alignment	not modelled	100.0	45	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
32	<a href="#">d2bs2a2</a>	Alignment	not modelled	100.0	43	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
33	<a href="#">d1jnra2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
34	<a href="#">c4cnjD_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> l-amino acid oxidase; <b>PDBTitle:</b> l-aminoacetone oxidase from streptococcus oligofermentans2 belongs to a new 3-domain family of bacterial flavoproteins
35	<a href="#">d1jnra1</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
36	<a href="#">c3g05B_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> crystal structure of n-terminal domain (2-550) of e.coli mnmg
37	<a href="#">c3cesB_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> crystal structure of e.coli mnmg (gida), a highly-conserved trna2 modifying enzyme
38	<a href="#">c3cp2A_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl <b>PDBTitle:</b> crystal structure of gida from e. coli
39	<a href="#">c3cp8C_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl <b>PDBTitle:</b> crystal structure of gida from chlorobium tepidum
40	<a href="#">d2gqfa1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
41	<a href="#">c3nlcA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein vp0956; <b>PDBTitle:</b> crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
42	<a href="#">c2zxiC_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> fad-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> structure of aquifex aeolicus gida in the form ii crystal
43	<a href="#">d1chua1</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> Spectrin repeat-like <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
44	<a href="#">d2bs2a3</a>	Alignment	not modelled	99.9	44	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
45	<a href="#">c2v6oA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase; <b>PDBTitle:</b> structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
46	<a href="#">c5w1jA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase; <b>PDBTitle:</b> echinococcus granulosus thioredoxin glutathione reductas (egtgr)
47	<a href="#">c1tytA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trypanothione reductase, oxidized form; <b>PDBTitle:</b> crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution
48	<a href="#">c3dqzA_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2; <b>PDBTitle:</b> crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
49	<a href="#">c1zkgA_</a>	Alignment	not modelled	99.9	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2, mitochondrial; <b>PDBTitle:</b> crystal structure of mouse thioredoxin reductase type 2
50	<a href="#">d1neka3</a>	Alignment	not modelled	99.9	46	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
51	<a href="#">d1kf6a3</a>	Alignment	not modelled	99.8	62	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase

51	<a href="#">c1ktv8B</a>	Alignment	not modelled	99.8	02	flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
52	<a href="#">c1hyuA</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> crystal structure of intact ahpf
53	<a href="#">d2i0za1</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
54	<a href="#">c5w4cA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase from cryptococcus2 neoformans in complex with fad (fo conformation)
55	<a href="#">c1zmcG</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
56	<a href="#">c1v59B</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
57	<a href="#">c2nvkX</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase from drosophila2 melanogaster
58	<a href="#">d1chua3</a>	Alignment	not modelled	99.8	40	<b>Fold:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Superfamily:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
59	<a href="#">c2w0hA</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trypanothione reductase; <b>PDBTitle:</b> x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
60	<a href="#">c2c3dB</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxopropyl-com reductase; <b>PDBTitle:</b> 2.15 angstrom crystal structure of 2-ketopropyl coenzyme m2 oxidoreductase carboxylase with a coenzyme m disulfide3 bound at the active site
61	<a href="#">c5odeA</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gll2934 protein; <b>PDBTitle:</b> structure of a novel oxidoreductase from gloeobacter violaceus
62	<a href="#">c5v36A</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> hydrolase,oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> 1.88 angstrom resolution crystal structure of glutathione reductase2 from streptococcus mutans ua159 in complex with fad
63	<a href="#">c6aonB</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> 1.72 angstrom resolution crystal structure of 2-oxoglutarate2 dehydrogenase complex subunit dihydrolipoamide dehydrogenase from3 bordetella pertussis in complex with fad
64	<a href="#">c5jriA</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase; <b>PDBTitle:</b> structure of an oxidoreductase semet-labelled from synechocystis sp.2 pcc6803
65	<a href="#">c1oijtA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> surface protein; <b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase
66	<a href="#">c2eq8E</a>	Alignment	not modelled	99.8	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
67	<a href="#">c4ntdA</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of hlmi
68	<a href="#">c1geuA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> oxidoreductase(flavoenzyme) <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> anatomy of an engineered nad-binding site
69	<a href="#">c4gcmB</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a thioredoxine reductase (trxb) from2 staphylococcus aureus subsp. aureus mu50 at 1.80 a resolution
70	<a href="#">c1ndaD</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> trypanothione oxidoreductase; <b>PDBTitle:</b> the structure of trypanosoma cruzi trypanothione reductase in the2 oxidized and nadph reduced state
71	<a href="#">c6b4oB</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> 1.73 angstrom resolution crystal structure of glutathione reductase2 from enterococcus faecalis in complex with fad
72	<a href="#">c2cfyB</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1; <b>PDBTitle:</b> crystal structure of human thioredoxin reductase 1
73	<a href="#">c5twcA</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> oxidoreductase iruo in the oxidized form
74	<a href="#">c3o0hA</a>	Alignment	not modelled	99.8	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of glutathione reductase from bartonella henselae
75	<a href="#">c6du7C</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> glutathione reductase from streptococcus pneumoniae

76	<a href="#">c3urhB</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
77	<a href="#">d3grsa1</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
78	<a href="#">c1ebdB</a>	Alignment	not modelled	99.8	27	<b>PDB header:</b> complex (oxidoreductase/transferase) <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
79	<a href="#">c1lpfB</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> three-dimensional structure of lipoamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties
80	<a href="#">c2zbwA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
81	<a href="#">c4dnaA</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable glutathione reductase; <b>PDBTitle:</b> crystal structure of putative glutathione reductase from sinorhizobium2 meliloti 1021
82	<a href="#">c2hqmB</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
83	<a href="#">c5wgyA</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-dependent halogenase; <b>PDBTitle:</b> crystal structure of mala' c112s/c128s, malbrancheamide b complex
84	<a href="#">c4j56A</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2; <b>PDBTitle:</b> structure of plasmodium falciparum thioredoxin reductase-thioredoxin2 complex
85	<a href="#">c2a8xA</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
86	<a href="#">c5uwvA</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> the crystal structure of thioredoxin reductase from streptococcus2 pyogenes mgas5005
87	<a href="#">d3lada1</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
88	<a href="#">c3atrA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> conserved archaeal protein; <b>PDBTitle:</b> geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
89	<a href="#">c1bwcA</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glutathione reductase); <b>PDBTitle:</b> structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
90	<a href="#">c5j60B</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> structure of a thioredoxin reductase from gloeobacter violaceus
91	<a href="#">c5x1yC</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> structure of mercuric reductase from lysinibacillus sphaericus
92	<a href="#">c6bwtD</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> 2.45 angstrom resolution crystal structure thioredoxin reductase from2 francisella tularensis.
93	<a href="#">c6gncA</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a ferredoxin-flavin thioredoxin reductase from2 clostridium acetobutylicum at 1.64 a resolution
94	<a href="#">c2q0IA</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
95	<a href="#">c6garB</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of oxidised ferredoxin/flavodoxin nadp+2 oxidoreductase 1 (fnr1) from bacillus cereus
96	<a href="#">c3jskN</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> N: <b>PDB Molecule:</b> cyppb37 protein; <b>PDBTitle:</b> thiazole synthase from neurospora crassa
97	<a href="#">c1dxC</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
98	<a href="#">d1lpfa1</a>	Alignment	not modelled	99.7	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
99	<a href="#">c4jmqA</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a thioredoxin reductase from brucella melitensis
100	<a href="#">c2eq7B</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e3 component; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> thioredoxin reductase;

101	<a href="#">c6gndG</a>	Alignment	not modelled	99.7	18	<b>PDBTitle:</b> crystal structure of the complex of a ferredoxin-flavin thioredoxin2 reductase and a thioredoxin from clostridium acetobutylicum at 2.9 a3 resolution
102	<a href="#">d1h6va1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
103	<a href="#">d1v59a1</a>	Alignment	not modelled	99.7	22	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
104	<a href="#">c6h3gC</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> alcohol oxidase; <b>PDBTitle:</b> alcohol oxidase from phanerochaete chrysosporium
105	<a href="#">c2r9zB</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione amide reductase; <b>PDBTitle:</b> glutathione amide reductase from chromatium gracile
106	<a href="#">c4jdrB</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase of pyruvate dehydrogenase from2 escherichia coli
107	<a href="#">c5xhuA</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ycgf from bacillus subtilis
108	<a href="#">d1feca1</a>	Alignment	not modelled	99.7	25	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
109	<a href="#">c3r9uA</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> thioredoxin-disulfide reductase from campylobacter jejuni.
110	<a href="#">c1f6mF</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a complex between thioredoxin reductase,2 thioredoxin, and the nadp+ analog, aadp+
111	<a href="#">c5yggB</a>	Alignment	not modelled	99.7	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ferredoxin nadp+ oxidoreductase from2 rhodopseudomonas palustris
112	<a href="#">c1m6iA</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 8; <b>PDBTitle:</b> crystal structure of apoptosis inducing factor (aif)
113	<a href="#">c1gthD</a>	Alignment	not modelled	99.7	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase; <b>PDBTitle:</b> dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
114	<a href="#">c4jnaA</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> deph; <b>PDBTitle:</b> crystal structure of the deph complex with dimethyl-fk228
115	<a href="#">c4fk1D</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative thioredoxin reductase; <b>PDBTitle:</b> crystal structure of putative thioredoxin reductase trxb from bacillus2 anthracis
116	<a href="#">c4ntcA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glit; <b>PDBTitle:</b> crystal structure of glit
117	<a href="#">c4a5iB</a>	Alignment	not modelled	99.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of the thioredoxin reductase from entamoeba2 histolytica
118	<a href="#">c2rghA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-glycerophosphate oxidase; <b>PDBTitle:</b> structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
119	<a href="#">c1lvA</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution
120	<a href="#">d1dxa1</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains